



IFW16

## RAW SEQUENCE LISTING

DATE: 08/31/2004

PATENT APPLICATION: US/09/889,182B

TIME: 13:51:20

Input Set : A:\4121-126\_third\_submission.ST25.txt

Output Set: N:\CRF4\08312004\I889182B.raw

3 <110> APPLICANT: Breitling, Frank  
 4 Poustka, Annemarie  
 5 Moldenhauer, Gerhard  
 7 <120> TITLE OF INVENTION: SELECTION OF MONOCLONAL ANTIBODIES  
 9 <130> FILE REFERENCE: 4121-126  
 11 <140> CURRENT APPLICATION NUMBER: US 09/889,182B  
 C--> 12 <141> CURRENT FILING DATE: 2002-01-10  
 14 <150> PRIOR APPLICATION NUMBER: PCT/DE00/00079  
 15 <151> PRIOR FILING DATE: 2000-01-11  
 17 <160> NUMBER OF SEQ ID NOS: 8  
 19 <170> SOFTWARE: PatentIn version 3.2  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 5732  
 23 <212> TYPE: DNA  
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 27 <223> OTHER INFORMATION: Synthetic sequence  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (737)..(1420)  
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 53 tgacgcaaat gggcggtagg cgtgtacggg gggaggtcta tataagcaga gctctctggc 600  
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 60 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu  
 61 1 5 10  
 63 ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat 820  
 64 Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp  
 65 15 20 25  
 67 tat gct ggg gcc caa aag ccc gag gtg atc gat gcc agc gag ctg acc 868  
 68 Tyr Ala Gly Ala Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr  
 69 30 35 40  
 71 ccc gcc gtg acc acc tac aag cta gtg atc aac ggc aag acc ctg aag 916

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72 Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys
73 45                               50                               55                               60
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76 Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
77                               65                               70                               75
79 ttc aaa caa tac gct aat gac aac ggg gtc gac ggc gag tgg act tac      1012
80 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
81                               80                               85                               90
83 gac gac gcc acc aag acc ttc acc gtg acc gag aag ccc gag gtg atc      1060
84 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
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87 gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag cta gtg atc      1108
88 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
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91 aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc gtg gac gcc      1156
92 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala
93 125                               130                               135                               140
95 gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac aac ggg gtc      1204
96 Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
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99 gac ggc gag tgg act tac gac gac gcc acc aag acc ttc acc gtg acc      1252
100 Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
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103 gag gcg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg      1300
104 Glu Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
105                               175                               180                               185
107 gcc gtc gac gga caa aac gac acc agc caa acc agc agc ccc tca gca      1348
108 Ala Val Asp Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala
109                               190                               195                               200
111 tcc agc aac ata agc gga ggc att ttc ctt ttc ttc gtg gcc aat gcc      1396
112 Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala
113 205                               210                               215                               220
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117                               225
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121 tctgttggtt gcccctcccc cgtgccttcc ttgacctgg aagggtgccac tcccactgtc      1570
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151	gcgagaaaa	aaaggatctc	aagaagatcc	tttgatcttt	tctacggggg	ctgacgctca	2470
153	gtggaacgaa	aactcacgtt	aagggatttt	ggcatgaga	ttatcaaaaa	ggatcttcac	2530
155	ctagatcctt	ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaacc	2590
157	tgaggctatg	gcagggcctg	ccgccccgac	gttggctgcg	agccctgggc	cttcaccgga	2650
159	acttgggggg	tggggtgggg	aaaaggaaga	aacgcgggcg	tattggcccc	aatgggggtc	2710
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163	cccaacaccg	tgcgttttat	tctgtctttt	tattgcccgc	atagcgcggg	ttccttcggg	2830
165	tattgtctcc	ttccgtgttt	cagttagcct	ccccctaggg	tgggcgaaga	actccagcat	2890
167	gagatccccg	cgctggagga	tcattccagcc	ggcgtcccgg	aaaacgattc	cgaagcccaa	2950
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231	aagatgcttt	tctgtgactg	gtgagtactc	aaccaagtca	ttctgagaat	agtgtatgcg	4870
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239	tactttcacc	agcgtttctg	ggtgagcaaa	aacaggaagg	caaaatgccg	caaaaaaggg	5110
241	aataagggcg	acacggaaat	gttgaatact	catactcttc	ctttttcaat	attattgaag	5170
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270 <223> OTHER INFORMATION: Synthetic Construct
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282 Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr
283 35 40 45
286 Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr
287 50 55 60
290 Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr
291 65 70 75 80
294 Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr
295 85 90 95
298 Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu
299 100 105 110
302 Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr
303 115 120 125
306 Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu
307 130 135 140
310 Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp
311 145 150 155 160
314 Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Ala Ala Ala
315 165 170 175
318 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly
319 180 185 190
322 Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile
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326 Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu
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340 <223> OTHER INFORMATION: Synthetic Sequence
343 <220> FEATURE:
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345 <222> LOCATION: (682)..(1782)
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368 taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga      660
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371                               Met Ala Pro Cys Met Leu Leu Leu Leu Leu
372                               1               5               10
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375 Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Gly Ala Gln Lys Glu
376                               15               20               25
378 aag acc ccc gag gag ccc aag gag gag gtg acc atc aag gcc aac ctg      807
379 Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu
380                               30               35               40
382 atc tac gcc gac ggc aag acc cag acc gcc gag ttc aag ggc acc ttc      855
383 Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe
384                               45               50               55
386 gag gag gcc acc gcg gag gcc tac cgc tac gcc gac gcc ctg aag aag      903
387 Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys
388                               60               65               70
390 gac aac ggc gag tac acc gtg gac gtg gcc gac aag ggc tac acc ctg      951
391 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu
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403 Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr
404                               125              130              135
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407 Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp
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**VERIFICATION SUMMARY**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date